

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Forderung der angewandten
Forschung e.V.

<120> Immunokinases

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<141> 2005-01-13

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<151> 2004-01-16

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<151> 2004-07-29

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<170> PatentIn version 3.5

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open reading frame (ORF)

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aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att	144
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Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg	
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gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg	336
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu	
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 260 265 270
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Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
 290 295 300
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 305 310 315 320
 His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala
 325 330 335
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 465 470 475 480
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 485 490 495
 Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser
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Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
Page 8

50

55

60

Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
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Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
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Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
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Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
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180 185 190

Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
195 200 205

Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
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Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser
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245 250 255

Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
260 265 270

Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
275 280 285

Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
290 295 300

Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
305 310 315 320

Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
325 330 335

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 Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His
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 Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val
 370 375 380
 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
 385 390 395 400
 Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
 405 410 415
 Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
 420 425 430
 Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
 435 440 445
 Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
 450 455 460
 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
 465 470 475 480
 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
 485 490 495
 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
 500 505 510
 Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe
 515 520 525
 Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
 530 535 540
 Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
 545 550 555 560
 Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro
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<220>
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1 5 10 15	
gcc cag ccg gcg atg gcc atg ggc cat cat cat cat cat cat cat cat	96
Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His	
20 25 30	
cat cac agc agc ggc cat atc gac gac gac gac aag cat atg aag ctt	144
His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu	
35 40 45	
atg gcc cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act	192
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr	
50 55 60	
gaa ctg gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct	240
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser	
65 70 75 80	
ggc tac acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct	288
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro	
85 90 95	
gga cag ggt ctg gaa tgg att gga tac att aat cct aac act gct tat	336
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr	
100 105 110	
act gac tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac	384
Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp	
115 120 125	
aaa tcc tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag	432
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu	
130 135 140	
gat tct gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg	480
Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp	
145 150 155 160	
ggg ttt cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt	528
Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly	
165 170 175	
gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att	576
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Gly Ser Asp Ile	
180 185 190	
gtg ctg acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg	624

Val	Leu	Thr 195	Gln	Ser	Pro	Lys	Ser 200	Met	Ala	Met	Ser	Val 205	Gly	Glu	Arg	
gtc Val	acc Thr	ttg Leu	agc Ser	tgc Cys	aag Lys	gcc Ala 215	agt Ser	gag Glu	aat Asn	gtg Val	gat Asp 220	tct Ser	ttt Phe	gtt Val	tcc Ser	672
tgg Trp 225	tat Tyr	caa Gln	cag Gln	aaa Lys	cca Pro 230	ggc Gly	cag Gln	tct Ser	cct Pro	aaa Lys 235	ctg Leu	ctg Leu	ata Ile	tac Tyr	ggg Gly 240	720
gcc Ala	tcc Ser	aac Asn	cgg Arg	tac Tyr 245	act Thr	ggg Gly	gtc Val	ccc Pro	gat Asp 250	cgc Arg	ttc Phe	gca Ala	ggc Gly	agt Ser 255	gga Gly	768
tct Ser	gga Gly	aga Arg	gat Asp 260	ttc Phe	act Thr	ctg Leu	acc Thr	atc Ile 265	agc Ser	agt Ser	gtg Val	cag Gln	gct Ala 270	gaa Glu	gac Asp	816
ctt Leu	gca Ala	gat Asp 275	tat Tyr	cac His	tgt Cys	gga Gly	cag Gln 280	aat Asn	tac Tyr	agg Arg	tat Tyr	ccg Pro 285	ctc Leu	acg Thr	ttc Phe	864
ggt Gly	gct Ala 290	ggc Gly	acc Thr	aag Lys	ctg Leu	gaa Glu 295	atc Ile	aaa Lys	cgg Arg	gcg Ala	gcc Ala 300	gca Ala	gag Glu	ctc Leu	ggc Gly	912
gga Gly 305	ggt Gly	ggc Gly	tct Ser	atg Met	gca Ala 310	gac Asp	gaa Glu	gat Asp	ctc Leu	atc Ile 315	ttc Phe	cgc Arg	ctg Leu	gaa Glu	ggc Gly 320	960
gtt Val	gat Asp	ggc Gly	ggc Gly	cag Gln 325	tcc Ser	ccc Pro	cga Arg	gct Ala	ggc Gly 330	cat His	gat Asp	ggt Gly	gat Asp	tct Ser 335	gat Asp	1008
ggg Gly	gac Asp	agc Ser	gac Asp 340	gat Asp	gag Glu	gaa Glu	ggt Gly	tac Tyr 345	ttc Phe	atc Ile	tgc Cys	ccc Pro	atc Ile 350	acg Thr	gat Asp	1056
gac Asp	cca Pro	agc Ser 355	tcg Ser	aac Asn	cag Gln	aat Asn	gtc Val 360	aat Asn	tcc Ser	aag Lys	gtt Val	aat Asn 365	aag Lys	tac Tyr	tac Tyr	1104
agc Ser	aac Asn 370	cta Leu	aca Thr	aaa Lys	agt Ser	gag Glu 375	cgg Arg	tat Tyr	agc Ser	tcc Ser	agc Ser 380	ggg Gly	tcc Ser	ccg Pro	gca Ala	1152
aac Asn 385	tcc Ser	ttc Phe	cac His	ttc Phe	aag Lys 390	gaa Glu	gcc Ala	tgg Trp	aag Lys	cac His 395	gca Ala	atc Ile	cag Gln	aag Lys	gcc Ala 400	1200
aag Lys	cac His	atg Met	ccc Pro	gac Asp 405	ccc Pro	tgg Trp	gct Ala	gag Glu	ttc Phe 410	cac His	ctg Leu	gaa Glu	gat Asp	att Ile 415	gcc Ala	1248
acc Thr	gaa Glu	cgt Arg	gct Ala 420	act Thr	cga Arg	cac His	agg Arg	tac Tyr 425	aac Asn	gcc Ala	gtc Val	acc Thr	ggg Gly 430	gaa Glu	tgg Trp	1296
ctg Leu	gat Asp	gat Asp 435	gaa Glu	gtt Val	ctg Leu	atc Ile	aag Lys 440	atg Met	gca Ala	tct Ser	cag Gln	ccc Pro 445	ttc Phe	ggc Gly	cga Arg	1344
gga Gly	gca Ala 450	atg Met	agg Arg	gag Glu	tgc Cys	ttc Phe 455	cgg Arg	acg Thr	aag Lys	aag Lys	ctc Leu 460	tcc Ser	aac Asn	ttc Phe	ttg Leu	1392
cat His	gcc Ala	cag Gln	cag Gln	tgg Trp	aag Lys	ggc Gly	gcc Ala	tcc Ser	aac Asn	tac Tyr	gtg Val	gcg Ala	aag Lys	cgc Arg	tac Tyr	1440

465						470						475						480	
atc Ile	gag Glu	ccc Pro	gta Val	gac Asp 485	cgg Arg	gat Asp	gtg Val	tac Tyr	ttt Phe 490	gag Glu	gac Asp	gtg Val	cgt Arg	cta Leu 495	cag Gln	1488			
atg Met	gag Glu	gcc Ala	aag Lys 500	ctc Leu	tgg Trp	ggg Gly	gag Glu	gag Glu 505	tat Tyr	aat Asn	cgg Arg	cac His	aag Lys 510	ccc Pro	ccc Pro	1536			
aag Lys	cag Gln	gtg Val 515	gac Asp	atc Ile	atg Met	cag Gln	atg Met 520	tgc Cys	atc Ile	atc Ile	gag Glu	ctg Leu 525	aag Lys	gac Asp	aga Arg	1584			
ccg Pro	ggc Gly 530	aag Lys	ccc Pro	ctc Leu	ttc Phe	cac His 535	ctg Leu	gag Glu	cac His	tac Tyr	atc Ile 540	gag Glu	ggc Gly	aag Lys	tac Tyr	1632			
atc Ile 545	aag Lys	tac Tyr	aac Asn	tcc Ser	aac Asn 550	tct Ser	ggc Gly	ttt Phe	gtc Val	cgc Arg 555	gat Asp	gac Asp	aac Asn	atc Ile	cgc Arg 560	1680			
ctg Leu	acg Thr	ccg Pro	cag Gln	gcc Ala 565	ttc Phe	agc Ser	cac His	ttc Phe	act Thr 570	ttt Phe	gag Glu	cgt Arg	tcc Ser	ggc Gly 575	cat His	1728			
cag Gln	ctg Leu	ata Ile	gtg Val 580	gtg Val	gac Asp	atc Ile	cag Gln	gga Gly 585	gtt Val	ggg Gly	gat Asp	ctc Leu	tac Tyr 590	act Thr	gac Asp	1776			
cca Pro	cag Gln	atc Ile 595	cac His	acg Thr	gag Glu	acg Thr	ggc Gly 600	act Thr	gac Asp	ttt Phe	gga Gly	gac Asp 605	ggc Gly	aac Asn	cta Leu	1824			
ggt Gly	gtc Val 610	cgc Arg	ggg Gly	atg Met	gcg Ala	ctc Leu 615	ttc Phe	ttc Phe	tac Tyr	tct Ser	cat His 620	gcc Ala	tgc Cys	aac Asn	cgg Arg	1872			
att Ile 625	tgc Cys	gag Glu	agc Ser	atg Met	ggc Gly 630	ctt Leu	gct Ala	ccc Pro	ttt Phe	gac Asp 635	ctc Leu	tcg Ser	ccc Pro	cgg Arg	gag Glu 640	1920			
agg Arg	gat Asp	gca Ala	gtg Val	aat Asn 645	cag Gln	aac Asn	acc Thr	aag Lys	ctg Leu 650	ctg Leu	caa Gln	tca Ser	gcc Ala	aag Lys 655	acc Thr	1968			
atc Ile	ttg Leu	aga Arg	gga Gly 660	aca Thr	gag Glu	gaa Glu	aaa Lys	tgt Cys 665	ggg Gly	agc Ser	ccc Pro	cga Arg	gta Val 670	agg Arg	acc Thr	2016			
ctc Leu	tct Ser	ggg Gly 675	agc Ser	cgg Arg	cca Pro	ccc Pro	ctg Leu 680	ctc Leu	cgt Arg	ccc Pro	ctt Leu	tca Ser 685	gag Glu	aac Asn	tct Ser	2064			
gga Gly 690	gac Asp	gag Glu	aac Asn	atg Met	agc Ser	gac Asp 695	gtg Val	acc Thr	ttc Phe	gac Asp 700	tct Ser 700	ctc Leu	cct Pro	tct Ser	tcc Ser	2112			
cca Pro 705	tct Ser	tcg Ser	gcc Ala	aca Thr	cca Pro 710	cac His	agc Ser	cag Gln	aag Lys	cta Leu 715	gac Asp	cac His	ctc Leu	cat His	tgg Trp 720	2160			
cca Pro	gtc Val	ttc Phe	agt Ser	gac Asp 725	ctc Leu	gat Asp	aac Asn	atg Met	gca Ala 730	tcc Ser	aga Arg	gac Asp	cat His	gat Asp 735	cat His	2208			
cta Leu	gac Asp	aac Asn	cac His 740	cgg Arg	gag Glu	tct Ser	gag Glu	aat Asn 745	agt Ser	ggg Gly	gac Asp	agc Ser	gga Gly 750	tac Tyr	ccc Pro	2256			

agt Ser	gag Glu	aag Lys 755	cgg Arg	ggg Gly	gag Glu	ctg Leu	gat Asp 760	gac Asp	cct Pro	gag Glu	ccc Pro	cga Arg 765	gaa Glu	cat His	ggc Gly	2304
cac His	tca Ser 770	tac Tyr	agt Ser	aat Asn	cgg Arg	aag Lys 775	tac Tyr	gag Glu	tct Ser	gac Asp	gaa Glu 780	gac Asp	agc Ser	ctg Leu	ggc Gly	2352
agc Ser 785	tct Ser	gga Gly	cgg Arg	gta Val	tgt Cys 790	gta Val	gag Glu	aag Lys	tgg Trp	aat Asn 795	ctc Leu	ctc Leu	aac Asn	tcc Ser	tcc Ser 800	2400
cgc Arg	ctc Leu	cac His	ctg Leu	ccg Pro 805	agg Arg	gct Ala	tcg Ser	gcc Ala	gtg Val 810	gcc Ala	ctg Leu	gaa Glu	gtg Val	caa Gln 815	agg Arg	2448
ctt Leu	aat Asn	gct Ala	ctg Leu 820	gac Asp	ctc Leu	gaa Glu	aag Lys	aaa Lys 825	atc Ile	ggg Gly	aag Lys	tcc Ser	att Ile 830	ttg Leu	ggg Gly	2496
aag Lys	gtc Val	cat His 835	ctg Leu	gcc Ala	atg Met	gtg Val	cgc Arg 840	tac Tyr	cac His	gag Glu	ggt Gly	ggg Gly 845	cgc Arg	ttc Phe	tgc Cys	2544
gag Glu	aag Lys 850	ggc Gly	gag Glu	gag Glu	tgg Trp	gac Asp 855	cag Gln	gag Glu	tcg Ser	gct Ala	gtc Val 860	ttc Phe	cac His	ctg Leu	gag Glu	2592
cac His 865	gca Ala	gcc Ala	aac Asn	ctg Leu	ggc Gly 870	gag Glu	ctg Leu	gag Glu	gcc Ala	atc Ile 875	gtg Val	ggc Gly	ctg Leu	gga Gly	ctc Leu 880	2640
atg Met	tac Tyr	tcg Ser	cag Gln	ttg Leu 885	cct Pro	cat His	cac His	atc Ile	cta Leu 890	gcc Ala	gat Asp	gtc Val	tct Ser	ctg Leu 895	aag Lys	2688
gag Glu	aca Thr	gaa Glu	gag Glu 900	aac Asn	aaa Lys	acc Thr	aaa Lys	gga Gly 905	ttt Phe	gat Asp	tac Tyr	tta Leu	cta Leu 910	aag Lys	gcc Ala	2736
gct Ala	gaa Glu	gct Ala 915	ggc Gly	gac Asp	agg Arg	cag Gln	tcc Ser 920	atg Met	atc Ile	cta Leu	gtg Val	gcg Ala 925	cga Arg	gct Ala	ttt Phe	2784
gac Asp	tct Ser 930	ggc Gly	cag Gln	aac Asn	ctc Leu	agc Ser 935	ccg Pro	gac Asp	agg Arg	tgc Cys	caa Gln 940	gac Asp	tgg Trp	cta Leu	gag Glu	2832
gcc Ala 945	ctg Leu	cac His	tgg Trp	tac Tyr	aac Asn 950	act Thr	gcc Ala	ctg Leu	gag Glu	atg Met 955	acg Thr	gac Asp	tgt Cys	gat Asp	gag Glu 960	2880
ggc Gly	ggt Gly	gag Glu	tac Tyr	gac Asp 965	gga Gly	atg Met	cag Gln	gac Asp	gag Glu 970	ccc Pro	cgg Arg	tac Tyr	atg Met 975	atg Met 975	ctg Leu	2928
gcc Ala	agg Arg	gag Glu	gcc Ala 980	gag Glu	atg Met	ctg Leu	ttc Phe	aca Thr 985	gga Gly	ggc Gly	tac Tyr	ggg Gly	ctg Leu 990	gag Glu	aag Lys	2976
gac Asp	ccg Pro	cag Gln 995	aga Arg	tca Ser	ggg Gly	gac Asp	ttg Leu 1000	tat Tyr	acc Thr	cag Gln	gca Ala	gca Ala 1005	gag Glu	gca Ala	gcg Ala	3024
atg Met	gaa Glu 1010	gcc Ala	atg Met	aag Lys	ggc Gly	cga Arg 1015	ctg Leu	gcc Ala	aac Asn	cag Gln	tac Tyr 1020	tac Tyr	caa Gln	aag Lys		3069

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 1025 1030

3102

<210> 6
 <211> 1033
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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 20 25 30

His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu
 35 40 45

Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr
 50 55 60

Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
 65 70 75 80

Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
 85 90 95

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
 100 105 110

Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp
 115 120 125

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu
 130 135 140

Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp
 145 150 155 160

Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 180 185 190

Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg
 195 200 205

Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser
 210 215 220

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly
 225 230 235 240
 Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly
 245 250 255
 Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
 260 265 270
 Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe
 275 280 285
 Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly
 290 295 300
 Gly Gly Gly Ser Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly
 305 310 315 320
 Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp
 325 330 335
 Gly Asp Ser Asp Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp
 340 345 350
 Asp Pro Ser Ser Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr
 355 360 365
 Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala
 370 375 380
 Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala
 385 390 395 400
 Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala
 405 410 415
 Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp
 420 425 430
 Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg
 435 440 445
 Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu
 450 455 460
 His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr
 465 470 475 480
 Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln
 485 490 495

Met Glu Ala Lys₅₀₀ Leu Trp Gly Glu Glu₅₀₅ Tyr Asn Arg His Lys₅₁₀ Pro Pro
 Lys Gln Val₅₁₅ Asp Ile Met Gln Met₅₂₀ Cys Ile Ile Glu Leu₅₂₅ Lys Asp Arg
 Pro Gly₅₃₀ Lys Pro Leu Phe His₅₃₅ Leu Glu His Tyr Ile₅₄₀ Glu Gly Lys Tyr
 Ile₅₄₅ Lys Tyr Asn Ser Asn₅₅₀ Ser Gly Phe Val Arg₅₅₅ Asp Asp Asn Ile Arg₅₆₀
 Leu Thr Pro Gln Ala₅₆₅ Phe Ser His Phe Thr₅₇₀ Phe Glu Arg Ser Gly₅₇₅ His
 Gln Leu Ile Val₅₈₀ Val Asp Ile Gln Gly₅₈₅ Val Gly Asp Leu Tyr₅₉₀ Thr Asp
 Pro Gln Ile₅₉₅ His Thr Glu Thr Gly₆₀₀ Thr Asp Phe Gly Asp₆₀₅ Gly Asn Leu
 Gly Val₆₁₀ Arg Gly Met Ala Leu₆₁₅ Phe Phe Tyr Ser His₆₂₀ Ala Cys Asn Arg
 Ile₆₂₅ Cys Glu Ser Met Gly₆₃₀ Leu Ala Pro Phe Asp₆₃₅ Leu Ser Pro Arg Glu₆₄₀
 Arg Asp Ala Val₆₄₅ Asn Gln Asn Thr Lys Leu₆₅₀ Leu Gln Ser Ala Lys₆₅₅ Thr
 Ile Leu Arg Gly₆₆₀ Thr Glu Glu Lys Cys₆₆₅ Gly Ser Pro Arg Val₆₇₀ Arg Thr
 Leu Ser Gly₆₇₅ Ser Arg Pro Pro Leu₆₈₀ Leu Arg Pro Leu Ser₆₈₅ Glu Asn Ser
 Gly Asp₆₉₀ Glu Asn Met Ser Asp₆₉₅ Val Thr Phe Asp Ser₇₀₀ Leu Pro Ser Ser
 Pro Ser Ser Ala Thr Pro₇₁₀ His Ser Gln Lys Leu₇₁₅ Asp His Leu His Trp₇₂₀
 Pro Val Phe Ser Asp₇₂₅ Leu Asp Asn Met Ala₇₃₀ Ser Arg Asp His Asp₇₃₅ His
 Leu Asp Asn His₇₄₀ Arg Glu Ser Glu Asn₇₄₅ Ser Gly Asp Ser Gly₇₅₀ Tyr Pro
 Ser Glu Lys₇₅₅ Arg Gly Glu Leu Asp₇₆₀ Asp Pro Glu Pro Arg₇₆₅ Glu His Gly

His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly
 770 775 780
 Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser
 785 790 795 800
 Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg
 805 810 815
 Leu Asn Ala Leu Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly
 820 825 830
 Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys
 835 840 845
 Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu
 850 855 860
 His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu
 865 870 875 880
 Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys
 885 890 895
 Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala
 900 905 910
 Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe
 915 920 925
 Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu
 930 935 940
 Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu
 945 950 955 960
 Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu
 965 970 975
 Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys
 980 985 990
 Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala
 995 1000 1005
 Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys
 1010 1015 1020
 Ala Glu Glu Ala Trp Ala Gln Met Glu Glu
 1025 1030

<210> 7

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic linker

<400> 7

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Myc epitope

<400> 8

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 9
<211> 6
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<220>
<223> motif in domain IX of kinases

<220>
<221> variant
<222> (2)..(2)
<223> Xaa is any amino acid

<220>
<221> variant
<222> (4)..(5)
<223> Xaa is any amino acid

<400> 9

Asp Xaa Trp Xaa Xaa Gly
1 5